

9	18	27	36	45	54
5' GGC TTC TGG GAG CNA CCG CTC CGC TCG TCT CGT TGG TTC CGG AGG TCG CTG CGG					
63	72	81	90	99	108
CGG TGG GAA ATG CTG GCG CGC GCG GCG CGG GGG CAC TGG GGC CCT TTT GCT GAG	M L A R A A R G H W G P F A E				
117	126	135	144	153	162
GGG CTC TCT ACT GGC TTC TGG CCG CGC TCC GGC CGC GCC TCC TCT GGA TTG CCC	G L S T G F W P R S G R A S S G L P				
171	180	189	198	207	215
CGA AAC ACC GTG GTA CTG TTC GTG CCG CAG CAG GAG GCC TGG GTG GTG GAG CGA	R N T V V L F V P Q Q E A W V V E R				
225	234	243	252	261	270
ATG GGC CGA TTC CAC CGG ATC CTG GAG CCT GGT TTG AAC ATC CTC ATC CCT GTG	M G R F H R I L E P G L N I L I P V				
279	288	297	306	315	324
TTA GAC CGG ATC CGA TAT GTG CAG AGT CTC AAG GAA ATT GTC ATC AAC GTG CCT	L D R I R Y V Q S L K E I V I N V P				
333	342	351	360	369	378
GAG CAG TCG GCT GTG ACT CTC GAC AAT GTA ACT CTG CAA ATC GAT GGA GTC CTT	E Q S A V T L D N V T L Q I D G V L				
387	396	405	414	423	432
TAC CTG CGC ATC ATG GAC CCT TAC AAG GCA AGC TAC GGT GTG GAG GAC CCT GAG	Y L R I M D P Y K A S Y G V E D P E				
441	450	459	468	477	486
TAT GCC GTC ACC CAG CTA GCT CAA ACA ACC ATG AGA TCA GAG CTC GGC AAA CTC	Y A V T Q L A Q T T M R S E L G K L				
495	504	513	522	531	540
TCT NTG GAC AAA GTC TTC CGG GAA CGG GAG TCC CTG AAT GCC AGC ATT GTG GAT	S X D K V F R E R E S L N A S I V D				
549	558	567	576	585	594
GCC ATC AAC CAA GCT GCT GAC TGC TGG GGT ATC CGC TGC CTN CGT TAT GAG ATC	A I N Q A A D C W G I R C L R Y E I				
603	612	621	630	639	648
AAG GAT ATC CAT GTG CCA CCC CGG GTG AAA GAG TCT ATG CAG ATG CAG GTG GAG	K D I H V P P R V K E S M Q M Q V E				
657	666	675	684	693	702
GCA GAG CGG CGG AAA CGG GCC ACA GTT CTA GAG TCT GAG GGG ACC CGA GAG TCG	A E R R K R A T V L E S E G T R E S				

FIGURE 1A

GCC	ATC	AAT	711	GTG	GCA	GAA	GGG	AAG	AAA	CAG	GCC	CAG	ATC	CTG	GCC	TCC	GAA	GCA	756
A	I	N	720	V	A	E	G	K	K	Q	A	Q	I	L	A	S	E	A	
GAA	AAG	GCT	765	GAA	CAG	ATA	AAT	CAG	GCA	GCA	GGA	GAG	GCC	AGT	GCA	GTT	CTG	GCG	810
E	K	A	774	E	Q	I	N	Q	A	A	G	E	A	S	A	V	L	A	
AAG	GCC	AAG	819	GCT	AAA	GCT	GAA	GCT	ATT	CGA	ATC	CTG	GCT	GCA	GCT	CTG	ACA	CAA	864
K	A	K	828	A	K	A	E	A	I	R	I	L	A	A	A	L	T	Q	
CAT	AAT	GGA	873	GAT	GCA	GCA	GCT	TCA	CTG	ACT	GTG	GCC	GAG	CAG	TAT	GTC	AGC	GCG	918
H	N	G	882	D	A	A	A	S	L	T	V	A	E	Q	Y	V	S	A	
TTC	TCC	AAA	927	CTG	GCC	AAG	GAC	TCC	AAC	ACT	ATC	CTA	CTG	CCC	TCC	AAC	CCT	GCG	972
F	S	K	936	L	A	K	D	S	N	T	I	L	L	P	S	N	P	G	
GAT	GTC	ACC	981	AGC	ATG	GTG	GCT	CAG	GCC	ATG	GGT	GTA	TAT	GGA	GCC	CTC	ACC	AAA	1026
D	V	T	990	S	M	V	A	Q	A	M	G	V	Y	G	A	L	T	K	
GCC	CCA	GTG	1035	CCA	GGG	ACT	CCA	GAC	TCA	CTC	TCC	AGT	GGG	AGC	AGC	AGA	GAT	GTC	1080
A	P	V	1044	P	G	T	P	D	S	L	S	S	G	S	S	R	D	V	
CAG	GGT	ACA	1089	GAT	GCA	AGT	NTT	GAT	GAG	GAA	CTT	GAT	CGA	GTC	AAG	ATG	AGT	TAG	1134
Q	G	T	1098	D	A	S	X	D	E	E	L	D	R	V	K	M	S	*	
TGG	AGC	TGG	1143	GCT	TNG	CCA	GGG	AGT	CTG	GGG	ACA	AGG	AAG	CAG	ATT	TTC	CTG	ATT	1188
			1152																
			1161																
			1170																
			1179																
			1188																

FIGURE 1B

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FIGURE 2A

148 R - - E R E S S N A S I V D A I N Q A A D C W G I R C L R Y E I K D I H V P P R 789094
 165 S - - D R E E I L A H N M Q S T L D D A T D A W G I K V E R V E I K D V K L P V Q GI 31069
 170 S - - D R E T I A S M Q T I L D E A T E S W G I K V E R V E I K D V R L P I Q GI 1065452
 197 S Q D R R I S A N L K D E L G S F T C Q F G V E I T D V E I S D V K I - - GI 1353669
 136 T - - S R D Q I N A Q L R G V L D E A T G R W G L R V A R V E L R S I D P P P S Z79701
 134 N - - K R E Y I N S K L L E I L D R E T D A W G V R I E K V E V K E I D P P E D GI 1591514

 186 V K E S M O M O V E A E R R K R A T V L E S E G T R E S A I N V A E G K K O A Q 789094
 203 L Q R A M A A E A E A S R E A R A K V I A A E G E M M A - - - - - GI 31069
 208 L Q R A M A A E A E A T R E A R A K V I A A E G E Q K A - - - - - GI 1065452
 234 V K E G E N M G M S A - - - - - L S S V A K S D A G Q Q L W Q GI 1353669
 174 I Q A S M E K Q M K A D R E K R A M I L T A E G T R E A A I K Q A E G Q K Q A Q Z79701
 172 I K N A M A Q Q M K A E R L K R A A I L E A E G E K P E GI 1591514

 226 I L A S E A E K A E Q I N Q A A G E A S A V L A K A K A K A E A I - - - - - 789094
 231 - - - - - - - - - - - S R A L K E A S M V I T E - - - - - GI 31069
 236 - - - - - - - - - - - S R A L R D A A S V I A Q - - - - - GI 1065452
 260 V I G P - - - - - V F E D F A K E C A A E K A K E N A P L V D L - - - - - GI 1353669
 214 I L A A E G A K Q A A I L A A E A D R Q S R M M L R A Q G E R A A A Y L Q A Q G Q Z79701

 259 - R I L A A A L T O H N G D A A A S L T V A E Q Y V S A F S K L A K D S N T I L 789094
 244 - - - - - - - - - - - S P A A L Q L R Y L Q T L T I A A E K N S T I GI 31069
 249 - - - - - - - - - - - S P A A L Q L R Y L Q T L N S V A R E K - - - - - GI 1065452
 288 S D V P S T S A A G T S T D T P N I P S I D I D H L I S V A S L A M D E H - L V GI 1353669
 254 A K A I E K T F A A I K A G R P T P E M L A Y Q Y L Q T L P E M A R G D A N K V Z79701

 298 - - - - - L P S N P G D V T S M V A Q A M - G V Y G A L T K A P V P G T P D 789094
 268 - - - - - V F E L P I D M - - - - - - - - - - - GI 31069
 269 - - - - - F D D H L P T - - - - - - - - - - - GI 1065452
 327 R L I G R V F Q I N C K D I E P - I C I D L K H G S G S A Y K G T S L - - N P D GI 1353669
 294 W V V P S D F N A A L Q G F T R L L G K P G E D G V F - R F E P S P V E D Q P K Z79701

FIGURE 2B

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FIGURE 2C

Library	Lib Description	Abun	Pct Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577
TESTNOT03	testis, 37 M	1	0.0557
LIVRNOT02	liver, 32 F	1	0.0515
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418
LVENNOT03	heart, left ventricle, 31 M	1	0.0336
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288
KERANOT01	keratinocytes, neonatal M	1	0.0227
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194
LUNGNOT04	lung, 2 M	1	0.0182
PGANNOT01	paraganglia, 46 M	1	0.0159
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150

FIGURE 3